

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/517,941A  
Source: IFWP  
Date Processed by STIC: 08/02/2006

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 08/02/2006

PATENT APPLICATION: US/10/517,941A

TIME: 09:03:58

Input Set : A:\0077 (OX40) Nov 11, 2005 version.ST25.txt

Output Set: N:\CRF4\08022006\J517941A.raw

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3 <110> APPLICANT: Crucell Holland B.V.
4     Bakker, Alexander B.H.
5     Meester-Rood, Pauline M.L.
6     Bakker, Adrianus Q.
8 <120> TITLE OF INVENTION: AGONISTIC BINDING MOLECULES TO THE HUMAN OX40 RECEPTOR
10 <130> FILE REFERENCE: 0077 WO 00 ORD
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/517,941A
C--> 12 <141> CURRENT FILING DATE: 2004-12-13
12 <150> PRIOR APPLICATION NUMBER: PCT/NL02/00389
13 <151> PRIOR FILING DATE: 2002-06-13
15 <160> NUMBER OF SEQ ID NOS: 54
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 769
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: scFv SC02008
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (3)..(767)
30 <223> OTHER INFORMATION: Source of genetic material is Homo sapiens
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39 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
40   20           25           30
42 agc aac tac acg atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg      143
43 Ser Asn Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
44   35           40           45
46 gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca      191
47 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
48   50           55           60
50 gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac      239
51 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
52   65           70           75
54 acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gtg      287
55 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
56 80           85           90           95
58 tat tac tgt gcc aaa gac cgc tac tcc cag gtg cac tac gcg ttg gat      335
59 Tyr Tyr Cys Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp

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64          115          120          125
66 tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac atc cag      431
67 Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln
68          130          135          140
70 atg acg cag tct cca gac tca ctg ccc gtc acc cct gga gag ccg gcc      479
71 Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
72          145          150          155
74 tcc atc tcc tgc agg tct agt cag agc ctc ctg cat agt aat gga tac      527
75 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
76 160          165          170          175
78 aac tat ttg gat tgg tac ctg cag aag gca ggg cag tct cca cag ctc      575
79 Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser Pro Gln Leu
80          180          185          190
82 ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc      623
83 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
84          195          200          205
86 agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc aga gtg      671
87 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
88          210          215          220
90 gag gct gag gat gtt ggg gtt tat tac tgc cag cag tac tac aac cac      719
91 Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn His
92          225          230          235
94 ccg acg acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc gcg gcc      767
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116          20          25          30
119 Asn Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
120          35          40          45
123 Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
124          50          55          60
127 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
128 65          70          75          80
131 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
132          85          90          95
135 Tyr Cys Ala Lys Asp Arg Tyr Ser Gln Val His Tyr Ala Leu Asp Tyr

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Output Set: N:\CRF4\08022006\J517941A.raw

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143 Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile Gln Met
144          130          135          140
147 Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser
148 145          150          155          160
151 Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn
152          165          170          175
155 Tyr Leu Asp Trp Tyr Leu Gln Lys Ala Gly Gln Ser Pro Gln Leu Leu
156          180          185          190
159 Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser
160          195          200          205
163 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu
164          210          215          220
167 Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr Tyr Asn His Pro
168 225          230          235          240
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186 <223> OTHER INFORMATION: Source of genetic material is Homo sapiens
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194 cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc      95
195 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
196 20 25 30
198 agc ggc tac tct atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg      143
199 Ser Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
200 35 40 45
202 gag tgg gtt ggc cgt act aga aac aaa gct aac agt tac acc aca gaa      191
203 Glu Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu
204 50 55 60
206 tac gcc gcg tct gtg aaa ggc aga ttc acc atc tca aga gat gat tca      239
207 Tyr Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
208 65 70 75
210 aag aac tca ctg tat ctg caa atg aac agt ctg aga gcc gag gac aca      287
211 Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
212 80 85 90 95
214 gcc gtg tat tac tgt gcc aaa gac cgc tac gtc aac acg tcg aac gcg      335

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215 Ala Val Tyr Tyr Cys Ala Lys Asp Arg Tyr Val Asn Thr Ser Asn Ala
216          100          105          110
218 ttc gat tac tgg ggc cag ggc acc ctg gtg acc gtg ctc gag ggt acc      383
219 Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr
220          115          120          125
222 gga ggt tcc ggc gga acc ggg tct ggg act ggt acg agc gag ctc gac      431
223 Gly Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp
224          130          135          140
226 atc cag atg aca cag tct cca gac tca ctg ccc gtc acc cct gga gag      479
227 Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu
228          145          150          155
230 ccg gcc tcc atc tcc tgc aga tct agt cag agc ctc ctg cat agt aat      527
231 Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn
232 160          165          170          175
234 gga tac aac tat ttg gat tgg tac ctg cag aag cca ggg cag tct cca      575
235 Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro
236          180          185          190
238 cag ctc ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc cct gac      623
239 Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp
240          195          200          205
242 agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc agc      671
243 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
244          210          215          220
246 aga gtg gag gct cac cat gtt ggg gtt tat tac tgc cag cag tac ccg      719
247 Arg Val Glu Ala His His Val Gly Val Tyr Tyr Cys Gln Gln Tyr Pro
248          225          230          235
250 ctg ggc ccg ccc acc ttc ggc cag ggc acc aaa ctg gaa atc aaa cgc      767
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277 Gly Tyr Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
278          35          40          45
281 Trp Val Gly Arg Thr Arg Asn Lys Ala Asn Ser Tyr Thr Thr Glu Tyr
282          50          55          60
285 Ala Ala Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys
286 65          70          75          80
289 Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala

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Output Set: N:\CRF4\08022006\J517941A.raw

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294          100          105          110
297 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Leu Glu Gly Thr Gly
298          115          120          125
301 Gly Ser Gly Gly Thr Gly Ser Gly Thr Gly Thr Ser Glu Leu Asp Ile
302          130          135          140
305 Gln Met Thr Gln Ser Pro Asp Ser Leu Pro Val Thr Pro Gly Glu Pro
306 145          150          155          160
309 Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly
310          165          170          175
313 Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln
314          180          185          190
317 Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg
318          195          200          205
321 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
322          210          215          220
325 Val Glu Ala His His Val Gly Val Tyr Tyr Cys Gln Gln Tyr Pro Leu
326 225          230          235          240
329 Gly Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala
330          245          250          255
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340 <213> ORGANISM: Artificial sequence
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345 <220> FEATURE:
346 <221> NAME/KEY: CDS
347 <222> LOCATION: (3)..(734)
348 <223> OTHER INFORMATION: Source of genetic material is Homo sapiens
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356 cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc 95
357 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
358 20 25 30
360 agc ggc tac cct atg aac tgg gtc cgc cag gcg ccc ggg aag ggg ctg 143
361 Ser Gly Tyr Pro Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
362 35 40 45
364 gag tgg gtg gca gtt ata tca tat gat gga agt aat aaa tac tac gca 191
365 Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
366 50 55 60
368 gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac 239
369 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
370 65 70 75
372 acg ctg tat ctg caa atg aac agc ctg aga gct gag gac aca gcc gtg 287

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**VERIFICATION SUMMARY**

DATE: 08/02/2006

PATENT APPLICATION: US/10/517,941A

TIME: 09:03:59

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date